IN THE CLAIMS:

Amend the claims as follows.

1. (Original) Method for isolating proteins involved in the recognition and targeted transport of a pathogenic virus circulating via the plasmodesmata in a plant, characterized in that samples containing complexes of said proteins with viral particles are subjected to electrophoresis and Western Blot using a capsid anti-protein monoclonal antibody, and the non-immunodetected bands are collected.

2. (Original) Method according to claim 1, characterized in that the complex is obtained from virus extracted from infected sensitive plants.

3. (Currently Amended) Method according to claim 2, characterized in that the virus is the Rice Yellow Mottle Virus (RYMV) ~~RYMV virus~~ and that proteins of 5, 24, 42, 49, 59, 66, 70, 77 and 210 kDa are collected.

4. (Original) Method according to claim 1, characterized in that the complex is obtained from purified virus and contacted with the proteins of a cell suspension of a sensitive plant.

5. (Currently Amended) Method according to claim 4, characterized in that the virus is the Rice Yellow Mottle Virus (RYMV) ~~RYMV virus~~, and that proteins of 24, 45, 51, 57, 63, 85 and beyond 120 kDa are collected.

6. (Previously Presented) Proteins such as obtained using the method according to claim 1.

7. (Original) Application of the proteins according to claim 6 for cloning resistance genes to pathogenic viruses circulating via the plasmodesmata in a plant.

8. (Original) cDNA corresponding to a protein according to claim 6, able to hybridize with a BAC clone screened from a bank containing DNA fragments of 100 to 150 kb of a rice variety such as IR64,for example a BAC bank (Bacterial Artifical Chromosomes), this BAC clone belonging to a contig, or group of BAC clones overlapping the region lying between the microsatellite markers RM252-RM272, of BAC clones containing the DNA sequences of markers identified from rice by means of a method comprising:

- selective amplification of rice DNA fragments firstly from resistant individuals, and secondly from sensitive individuals, descending from parental varieties, these fragments being previously subjected to a digestion step, then a ligation step to fix complementary primer adapters having at their end one or more specific nucleotides, one the primers of the pair being labelled for development purposes,

- separation of the amplification products, by gel electrophoresis under denaturing conditions, and

- comparison of the electrophoresis profiles obtained with mixtures of fragments derived from resistant descendants and mixtures derived from sensitive descendants, with fragments derived from parental varieties, for the purpose of identifying bands

whose polymorphism is genetically linked to the resistance locus, this identification optionally being followed, for validation purposes, by verification on each individual and calculation of the genetic recombination rate between the marker and the resistance locus.

9. (Original) cDNA according to claim 8, characterized in that said polymorphous AFLP bands are specifically evidenced in a variety sensitive to RYMV, and in the fraction of sensitive plants derived from the crossing of this variety with the resistant *Gigante* variety.

10. (Previously Presented) cDNA according to claim 8, characterized in that said DNA sequences corresponding to said polymorphous bands, carry the RYMV resistance locus and define a segment of less than 10cM.

11. (Original) cDNA according to claim 10, characterized in that said DNA sequences are EcoRI-MseI fragments.

12. (Original) cDNA according to claim 11, characterized in that the size of said fragments is respectively 510 bp and 140 bp at gel electrophoresis under denaturing conditions.

13. (Previously Presented) cDNA according to claim 8, characterized in that said DNA fragments correspond to DNA sequences flanking the resistance locus and located either side of the latter at 5-10cM.

14. (Original) cDNA according to claim 13, characterized in that a DNA sequence is used meeting SEQ ID N°3 or SEQ ID N°9.